

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:59:19 ; Search time 59.03 Seconds

(without alignments)
90.849 Million cell updates/sec

Title: US-09-785-059-2

Perfect score: 148
Sequence: 1 RVIRVORACRAIRHVRIRIGRLRVV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	75.7	854	15	056319 simian-huma
2	112	75.7	856	15	092877 simian-huma
3	112	75.7	856	15	074599 human immun
4	112	75.7	856	15	090587 human immun
5	111	75.0	854	15	089797 human immun
6	111	75.0	854	15	092762 human immun
7	110	74.3	856	15	077694 human immun
8	110	74.3	859	15	09JAC1 human immun
9	107	72.3	866	15	073301 human immun
10	106	71.6	855	15	074841 human immun
11	106	71.6	858	15	092874 human immun
12	106	71.6	859	15	092937 human immun
13	105	70.9	853	15	056108 human immun
14	105	70.9	860	15	09DH01 human immun
15	105	70.9	861	15	09E527 human immun
16	105	70.9	861	15	09E523 human immun

17	105	70.9	862	15	093024 human immun
18	104	70.3	860	15	09E534 human immun
19	104	70.3	860	15	09E518 human immun
20	104	70.3	872	15	091U21 human immun
21	104	70.3	872	15	091U20 human immun
22	103	69.6	357	15	078100 human immun
23	103	69.6	853	15	056563 human immun
24	103	69.6	856	15	074090 human immun
25	103	69.6	862	15	09DVL5 human immun
26	102	68.9	849	15	09PXE5 human immun
27	102	68.9	853	15	073372 human immun
28	102	68.9	858	15	071974 human immun
29	102	68.9	858	15	091U25 human immun
30	102	68.9	859	15	P87924 human immun
31	101	68.2	136	15	079566 human immun
32	101	68.2	851	15	078243 human immun
33	101	68.2	861	15	091U24 human immun
34	101	68.2	869	15	073302 human immun
35	101	68.2	869	15	090RE5 human immun
36	101	68.2	883	15	090RE5 human immun
37	100	67.6	856	15	0902G3 human immun
38	100	67.6	860	15	073309 human immun
39	100	67.6	863	15	041552 human immun
40	99	66.9	56	15	056181 human immun
41	99	66.9	56	15	056182 human immun
42	99	66.9	56	15	056183 human immun
43	99	66.9	56	15	056184 human immun
44	99	66.9	56	15	056185 human immun
45	99	66.9	56	15	056199 human immun

ALIGNMENTS

RESULT 1
ID 056319 PRELIMINARY: PRT: 854 AA.
AC 056319;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ENV.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHIV-89.6;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P., Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G., Sodroski J., Letvin N.L.;
RT "An env gene derived from a primary human immunodeficiency virus type 1 isolate confers high in vivo replicative capacity to a chimeric simian/human immunodeficiency virus in rhesus monkeys";
RT J. Virol. 70:3198-3206(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SHIV-89.6;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P., Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G., Sodroski J., Letvin N.L.;
RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF038398; AAB9966.1; -;
DR InterPro: IPR00328; Env_Gp41.
DR InterPro: IPR00777; Gp120.
DR Pfam: PF00516; Gp120; 1.
DR Pfam: PF00517; Gp41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ .SEQUENCE 854 AA: 97265 MW: 72AAB153IDCEAF7 CRC64;

Query Match 75.7%; Score 112; DB 15; Length 856;
 Best Local Similarity 85.7%; Pred. No. 3.8e-07;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVIRVORACRAIRHIVRIRIGLRIL 28
 DB 828 RVIEVVGACRAIRHIVRIRIGLRIL 853

RESULT 2

092877 PRELIMINARY; PRT; 856 AA.
 AC 092877;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Simian-Human immunodeficiency virus.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=57667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9098984; PubMed=9882298;
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
 RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,
 RA Sodroski J.G.;
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
 responsible for the pathogenicity of a multiply passaged simian-human
 immunodeficiency virus (SHIV-HXB2).";
 RT J. Virol. 73:976-984(1999).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF041850; AAD12142.1; -;
 DR InterPro: IPR000328; Env_GPA1.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GPA1; 1.
 KM AIDS. Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;

Query Match 75.7%; Score 112; DB 15; Length 856;
 Best Local Similarity 85.7%; Pred. No. 3.8e-07;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVIRVORACRAIRHIVRIRIGLRIL 28
 DB 828 RVIEVVGACRAIRHIVRIRIGLRIL 855

RESULT 3
 074599 PRELIMINARY; PRT; 856 AA.

AC 074599;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ENV.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-MCK1;
 RX MEDLINE=9011366; PubMed=1688473;
 RA Cloyd M.W., Moore B.E.;
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
 (HIV-1) Isolates.";

RL Virology 174:103-116(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MCK1;

RA Itatani Y.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D86066; BAA12995.1; -;
 DR InterPro: IPR000328; Env_GPA1.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GPA1; 1.
 KM AIDS. Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;

Query Match 75.7%; Score 112; DB 15; Length 856;
 Best Local Similarity 85.7%; Pred. No. 3.8e-07;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVIRVORACRAIRHIVRIRIGLRIL 28
 DB 828 RVIEVVGACRAIRHIVRIRIGLRIL 855

RESULT 4
 090SM7 PRELIMINARY; PRT; 856 AA.

AC 090SM7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HXB2;
 RA Ataman-Onal Y., Cheynet V., Verrier B.;
 RT "Mutations and transcriptional alterations associated with the
 RT downregulation of HIV-1 envelope glycoprotein expression following
 RT acute cytopathic effects.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF58141; AAK49977.1; -;
 SQ SEQUENCE 856 AA; 97126 MW; 9458D02B2FD734B3 CRC64;

Query Match 75.7%; Score 112; DB 15; Length 856;
 Best Local Similarity 85.7%; Pred. No. 3.8e-07;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVIRVORACRAIRHIVRIRIGLRIL 28
 DB 828 RVIEVVGACRAIRHIVRIRIGLRIL 855

RESULT 5
 089797 PRELIMINARY; PRT; 852 AA.

AC 089797;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LM90-2;
 RX MEDLINE=95127297; PubMed=7826699;

AC 073301;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96263682; PubMed=8924250;
 RA Douglas N.W., Knight A.I., Hayhurst A., Barrett W.Y., Kevany M.J., Daniels R.S.;
 RT "An efficient method for the rescue and analysis of functional HIV-1 env genes: evidence for recombination in the vicinity of the tat/rev splice site."
 RL AIDS 10:39-46(1996).
 DR EMBL; U36875; AAC5535.1; -.
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 866 AA; 98348 MW; 6482AF2FED4BD4A0 CRC64;

Query Match 72.3%; Score 107; DB 15; Length 866;
 Best Local Similarity 75.9%; Pred. No. 1.8e-06;
 Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RVIRVORACRAIRHIVRIRIROGLRRL 29
 |||:||||||| || ||||| | | |
 Db 838 RVIEVGRACRAIRHIVRIRIROGLRRLQ 866

RESULT 10
 ID 074841 PRELIMINARY; PRT; 855 AA.
 AC 074841;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ENV.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90303973; PubMed=2364020;
 RA Suetschman U., Schneider J., Mous J., Brunckhorst U., Schedel I., Jentsch K.D., Hunsmann G.;
 RT "Molecular cloning and characterization of a German HIV-1 isolate."
 RL AIDS Res. Hum. Retroviruses 6:813-823(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HAN-2;
 RA Bryant B.W.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U43141; AAA85237.1; -.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 855 AA; 97507 MW; EF3CB615A2392F9 CRC64;

Qy 1 RVIRVORACRAIRHIVRIRIROGLRRL 28
 |||:||||||| || ||||| | | |
 Db 827 RVIEVGRACRAIRHIVRIRIROGLRRL 854

RESULT 11
 ID 092874 PRELIMINARY; PRT; 858 AA.
 AC 092874;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHI146;
 RX MEDLINE=99372987; PubMed=10445815;
 RA Ataman-Onal Y., Collier C., Giraud A., Babic-Erceg A., Biton F., Verrier B.;
 RT "Comparison of complete env gene sequences from individuals with symptomatic primary HIV type 1 infection."
 RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
 DR EMBL; AF041127; AAC02518.1; -.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 858 AA; 97396 MW; 8E43A641C9D1535F CRC64;

Query Match 71.6%; Score 106; DB 15; Length 856;
 Best Local Similarity 78.6%; Pred. No. 2.5e-06;
 Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RVIRVORACRAIRHIVRIRIROGLRRL 28
 |||:||||||| || ||||| | | |
 Db 830 RVIEVGRACRAIRHIVRIRIROGLRRL 857

RESULT 12
 ID 092937 PRELIMINARY; PRT; 859 AA.
 AC 092937;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIV-1JC;
 RX MEDLINE=98440562; PubMed=9765443;
 RA Weng D.M., Novembre F.J.;
 RT "Molecular cloning and characterization of viruses isolated from chimpanzees with pathogenic human immunodeficiency virus type 1 infections."
 RL J. Virol. 72:8976-8987(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIV-1JC;
 RA Weng D.M., Novembre F.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF049494; AAC68848.1; -.
 DR InterPro: IPR000328; Env_GP41.

